



PCT10

## RAW SEQUENCE LISTING

DATE: 04/17/2002

PATENT APPLICATION: US/10/089,485

TIME: 12:16:40

Input Set : A:\62489.txt

Output Set: N:\CRF3\04172002\J089485.raw

**ENTERED**

3 <110> APPLICANT: Hanada and Yang  
 5 <120> TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-5 (FGF-5) IS A TUMOR  
 6 ASSOCIATED T-CELL ANTIGEN  
 8 <130> FILE REFERENCE: 55911  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/089,485  
 C--> 11 <141> CURRENT FILING DATE: 2002-03-27  
 13 <150> PRIOR APPLICATION NUMBER: PCT/US00/26689  
 14 <151> PRIOR FILING DATE: 2000-09-29  
 16 <150> PRIOR APPLICATION NUMBER: 60/157,103  
 17 <151> PRIOR FILING DATE: 1999-10-02  
 19 <160> NUMBER OF SEQ ID NOS: 25  
 21 <170> SOFTWARE: PatentIn Ver. 2.1  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 143  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Homo sapiens  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (27)..(140)  
 32 <400> SEQUENCE: 1  
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 34 Met Ser Thr Arg Cys Gly Glu Ala Gly  
 35 1 5  
 37 aga gcc aga ggc acg cag ccg cac agg ggc tac aga gcc cag aat caa 101  
 38 Arg Ala Arg Gly Thr Gln Pro His Arg Gly Tyr Arg Ala Gln Asn  
 39 10 15 20  
 41 ccc tac aag atg cac tta gga ccc ccg cgg ctg gaa gaa tga 143  
 42 Pro Tyr Lys Met His Leu Gly Pro Pro Arg Leu Glu Glu  
 43 30 35  
 46 <210> SEQ ID NO: 2  
 47 <211> LENGTH: 38  
 48 <212> TYPE: PRT  
 49 <213> ORGANISM: Homo sapiens  
 51 <400> SEQUENCE: 2  
 52 Met Ser Thr Arg Cys Gly Glu Ala Gly Arg Ala Arg Gly Thr Gln Pro  
 53 1 5 10 15  
 55 His Arg Gly Tyr Arg Ala Gln Asn Gln Pro Tyr Lys Met His Leu Gly  
 56 20 25 30  
 58 Pro Pro Arg Leu Glu Glu  
 59 35  
 63 <210> SEQ ID NO: 3  
 64 <211> LENGTH: 1123  
 65 <212> TYPE: DNA

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66 &lt;213&gt; ORGANISM: Homo sapiens

68 &lt;220&gt; FEATURE:

69 &lt;221&gt; NAME/KEY: CDS

70 &lt;222&gt; LOCATION: (140)..(946)

72 &lt;400&gt; SEQUENCE: 3

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73 cctctccctt tctcttcccc gaggtatgt ccacccggtg cggcgaggcg ggcagagcca 60
75 gaggcacgca gccgcacagg ggctacagag ccagaaatca gccctacaag atgcacttag 120
77 gacccccgcg gctggaaga atg agc ttg tcc ttc ctc ctc ctc ctc ttc ttc 172
78                               Met Ser Leu Ser Phe Leu Leu Leu Leu Phe Phe
79                               1             5             10
81 agc cac ctg atc ctc agc gcc tgg gct cac ggg gag aag cgt ctc gcc 220
82 Ser His Leu Ile Leu Ser Ala Trp Ala His Gly Glu Lys Arg Leu Ala
83                               15             20             25
85 ccc aaa ggg caa ccc gga ccc gct gcc act gat agg aac cct ata ggc 268
86 Pro Lys Gly Gln Pro Gly Pro Ala Ala Thr Asp Arg Asn Pro Ile Gly
87                               30             35             40
89 tcc agc agc aga cag agc agc agt agc gct atg tct tcc tct tct gcc 316
90 Ser Ser Ser Arg Gln Ser Ser Ser Ser Ala Met Ser Ser Ser Ser Ala
91                               45             50             55
93 tcc tcc tcc ccc gca gct tct ctg ggc agc caa gga agt ggc ttg gag 364
94 Ser Ser Ser Pro Ala Ala Ser Leu Gly Ser Gln Gly Ser Gly Leu Glu
95 60                               65             70             75
97 cag agc agt ttc cag tgg agc ccc tgg ggg cgc cgg acc ggc agc ctc 412
98 Gln Ser Ser Phe Gln Trp Ser Pro Ser Gly Arg Arg Thr Gly Ser Leu
99                               80             85             90
101 tac tgc aga gtg ggc atc ggt ttc cat ctg cag atc tac ccg gat ggc 460
102 Tyr Cys Arg Val Gly Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly
103                               95             100            105
105 aaa gtc aat gga tcc cac gaa gcc aat atg tta agt gtt ttg gaa ata 508
106 Lys Val Asn Gly Ser His Glu Ala Asn Met Leu Ser Val Leu Glu Ile
107                               110            115            120
109 ttt gct gtg tct cag ggg att gta gga ata cga gga gtt ttc agc aac 556
110 Phe Ala Val Ser Gln Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn
111                               125            130            135
113 aaa ttt tta gcg atg tca aaa aaa gga aaa ctc cat gca agt gcc aag 604
114 Lys Phe Leu Ala Met Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys
115 140                               145            150            155
117 ttc aca gat gac tgc aag ttc agg gag cgt ttt caa gaa aat agc tat 652
118 Phe Thr Asp Asp Cys Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr
119                               160            165            170
121 aat acc tat gcc tca gca ata cat aga act gaa aaa aca ggg cgg gag 700
122 Asn Thr Tyr Ala Ser Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu
123                               175            180            185
125 tgg tat gtt gcc ctg aat aaa aga gga aaa gcc aaa cga ggg tgc agc 748
126 Trp Tyr Val Ala Leu Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser
127                               190            195            200
129 ccc cgg gtt aaa ccc cag cat atc tct acc cat ttt ctt cca aga ttc 796
130 Pro Arg Val Lys Pro Gln His Ile Ser Thr His Phe Leu Pro Arg Phe
131                               205            210            215

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133 aag cag tcg gag cag cca gaa ctt tct ttc acg gtt act gtt cct gaa      844
134 Lys Gln Ser Glu Gln Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu
135 220                225                230                235
137 aag aaa aat cca cct agc cct atc aag tca aag att ccc ctt tct gca      892
138 Lys Lys Asn Pro Pro Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala
139                240                245                250
141 cct cgg aaa aat acc aac tca gtg aaa tac aga ctc aag ttt cgc ttt      940
142 Pro Arg Lys Asn Thr Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe
143                255                260                265
145 gga taa tattaatctt ggccttgtga gaaaccattc tttccctca ggagtttcta      996
146 Gly
148 taggtgtctt cagagttctg aagaaaaatt actggacaca gcttcagcta tacttacact 1056
150 gtattgaagt caggtcattt gtttcagtgt gactgaaaca aaatgttttt tgataggaag 1116
152 gaaactg                                     1123
155 <210> SEQ ID NO: 4
156 <211> LENGTH: 268
157 <212> TYPE: PRT
158 <213> ORGANISM: Homo sapiens
160 <400> SEQUENCE: 4
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162 1          5          10          15
163 Ser Ala Trp Ala His Gly Glu Lys Arg Leu Ala Pro Lys Gly Gln Pro
164          20          25          30
165 Gly Pro Ala Ala Thr Asp Arg Asn Pro Ile Gly Ser Ser Ser Arg Gln
166          35          40          45
167 Ser Ser Ser Ser Ala Met Ser Ser Ser Ser Ala Ser Ser Ser Pro Ala
168          50          55          60
169 Ala Ser Leu Gly Ser Gln Gly Ser Gly Leu Glu Gln Ser Ser Phe Gln
170 65          70          75          80
171 Trp Ser Pro Ser Gly Arg Arg Thr Gly Ser Leu Tyr Cys Arg Val Gly
172          85          90          95
173 Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys Val Asn Gly Ser
174          100         105         110
175 His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe Ala Val Ser Gln
176          115         120         125
177 Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys Phe Leu Ala Met
178          130         135         140
179 Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe Thr Asp Asp Cys
180 145         150         155         160
181 Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn Thr Tyr Ala Ser
182          165         170         175
183 Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp Tyr Val Ala Leu
184          180         185         190
185 Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser Pro Arg Val Lys Pro
186          195         200         205
187 Gln His Ile Ser Thr His Phe Leu Pro Arg Phe Lys Gln Ser Glu Gln
188          210         215         220
189 Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu Lys Lys Asn Pro Pro
190 225         230         235         240

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191 Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala Pro Arg Lys Asn Thr
192                245                250                255
193 Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe Gly
194                260                265
198 <210> SEQ ID NO: 5
199 <211> LENGTH: 531
200 <212> TYPE: DNA
201 <213> ORGANISM: Homo sapiens
203 <220> FEATURE:
204 <221> NAME/KEY: CDS
205 <222> LOCATION: (1)..(531)
207 <400> SEQUENCE: 5
208 tgc aga gtg ggc atc ggt ttc cat ctg cag atc tac ccg gat ggc aaa      48
209 Cys Arg Val Gly Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys
210   1          5          10          15
212 gtc aat gga tcc cac gaa gcc aat atg tta agt gtt ttg gaa ata ttt      96
213 Val Asn Gly Ser His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe
214                20                25                30
216 gct gtg tct cag ggg att gta gga ata cga gga gtt ttc agc aac aaa      144
217 Ala Val Ser Gln Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys
218                35                40                45
220 ttt tta gcg atg tca aaa aaa gga aaa ctc cat gca agt gcc aag ttc      192
221 Phe Leu Ala Met Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe
222                50                55                60
224 aca gat gac tgc aag ttc agg gag cgt ttt caa gaa aat agc tat aat      240
225 Thr Asp Asp Cys Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn
226   65          70          75          80
228 acc tat gcc tca gca ata cat aga act gaa aaa aca ggg cgg gag tgg      288
229 Thr Tyr Ala Ser Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp
230                85                90                95
232 tat gtt gcc ctg aat aaa aga gga aaa gcc aaa cga ggg tgc agc ccc      336
233 Tyr Val Ala Leu Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser Pro
234                100               105               110
236 cgg gtt aaa ccc cag cat atc tct acc cat ttt ctt cca aga ttc aag      384
237 Arg Val Lys Pro Gln His Ile Ser Thr His Phe Leu Pro Arg Phe Lys
238                115               120               125
240 cag tcg gag cag cca gaa ctt tct ttc acg gtt act gtt cct gaa aag      432
241 Gln Ser Glu Gln Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu Lys
242                130               135               140
244 aaa aat cca cct agc cct atc aag tca aag att ccc ctt tct gca cct      480
245 Lys Asn Pro Pro Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala Pro
246  145          150          155          160
248 cgg aaa aat acc aac tca gtg aaa tac aga ctc aag ttt cgc ttt gga      528
249 Arg Lys Asn Thr Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe Gly
250                165               170               175
252 taa                                                                531
256 <210> SEQ ID NO: 6
257 <211> LENGTH: 176
258 <212> TYPE: PRT

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259 <213> ORGANISM: Homo sapiens
261 <400> SEQUENCE: 6
262 Cys Arg Val Gly Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys
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264 Val Asn Gly Ser His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe
265           20           25           30
266 Ala Val Ser Gln Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys
267           35           40           45
268 Phe Leu Ala Met Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe
269           50           55           60
270 Thr Asp Asp Cys Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn
271   65           70           75           80
272 Thr Tyr Ala Ser Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp
273           85           90           95
274 Tyr Val Ala Leu Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser Pro
275           100          105          110
276 Arg Val Lys Pro Gln His Ile Ser Thr His Phe Leu Pro Arg Phe Lys
277           115          120          125
278 Gln Ser Glu Gln Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu Lys
279           130          135          140
280 Lys Asn Pro Pro Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala Pro
281 145           150          155          160
282 Arg Lys Asn Thr Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe Gly
283           165          170          175
287 <210> SEQ ID NO: 7
288 <211> LENGTH: 531
289 <212> TYPE: DNA
290 <213> ORGANISM: Homo sapiens
292 <220> FEATURE:
293 <221> NAME/KEY: CDS
294 <222> LOCATION: (1)..(531)
296 <400> SEQUENCE: 7
297 tgc aga gtg ggc atc ggt ttc cat ctg cag atc tac ccg gat ggc aaa 48
298 Cys Arg Val Gly Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys
299   1           5           10           15
301 gtc aat gga tcc cac gaa gcc aat atg tta agt gtt ttg gaa ata ttt 96
302 Val Asn Gly Ser His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe
303           20           25           30
305 gct gtg tct cag ggg att gta gga ata cga gga gtt ttc agc aac aaa 144
306 Ala Val Ser Gln Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys
307           35           40           45
309 ttt tta gcg atg tca aaa aaa gga aaa ctc cat gca agt gcc aag ttc 192
310 Phe Leu Ala Met Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe
311           50           55           60
313 aca gat gac tgc aag ttc agg gag cgt ttt caa gaa aat agc tat aat 240
314 Thr Asp Asp Cys Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn
315   65           70           75           80
317 acc tat gcc tca gca ata cat aga act gaa aaa aca ggg cgg gag tgg 288
318 Thr Tyr Ala Ser Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp

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VERIFICATION SUMMARY

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Input Set : A:\62489.txt

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L:11 M 271 C: Current Filing Date differs, Replaced Current Filing Date